Metabolic pathway extraction using combined probabilistic models

Abstract:

Extracting metabolic pathway from microarray gene expression data that dictates a specific biological response is currently one of the important disciplines in system biology research. However due to the complexity of the global metabolic network and the importance to maintain the biological structure, this has become a greater challenge. Previous methods have successfully identified those pathways but without concerning the genetic effect and relationship of the genes, representation of the underlying structure is not precise and cannot be justified to be significant biologically. In this article, probabilistic models that are capable of identifying the significant pathways through metabolic networks related to a specific biological response are implemented. This article utilized combination of two probabilistic models to address the limitations of previous methods with the annotation to pathway database to ensure the pathway is biologically plausible.